

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 25, 2001, 09:26:12 ; Search time 22.69 Seconds
(without alignments)
1265.577 Million cell

Title: US-09-829-931-2
 Perfect score: 1298
 Sequence: 1 MKNWYRIKXVVIIGPFLRV.....DVKNALIEEGKYCEGTAPSO 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Minimum	DB seq	length:
Maximum	DB seq	length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :
SPTRMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1298	100.0	245	2	Q9KKE6	Q9KKE6 corynebacte
2	575	44.3	245	2	O69572	O69572 mycobacteri
3	566	43.6	247	2	O53516	O53516 mycobacteri
4	499	38.4	262	2	Q9S2M2	Q9S2M2 streptomyc
5	478	36.8	223	2	Q9L1B5	Q9L1B5 streptomyc
6	413	31.8	199	2	Q33970	Q33970 streptomyc
7	252.5	19.5	211	2	O67841	O67841 aquifex ae
8	246.5	19.0	247	2	Q9X219	Q9X219 thermotoga
9	226	17.4	823	2	O67119	O67119 aquifex ae
10	223	17.2	216	2	Q9PJT9	Q9PJT9 chlamydia m
11	217.5	16.8	264	2	Q9ZBS1	Q9ZBS1 streptomyc
12	215.5	16.6	195	2	Q9KCD7	Q9KCD7 bacillus ha
13	212.5	16.4	225	2	P74498	P74498 synecocyst
14	212.5	16.3	216	2	O84459	O84459 chlamydia t
15	202	15.6	212	10	Q9M0A2	Q9M0A2 arabidopsis
16	181	13.9	344	10	Q9LLF4	Q9LLF4 brassica na
17	173.5	13.4	259	2	O07807	O07807 mycobacteri
18	171.5	13.2	355	2	Q9WX09	Q9WX09 streptomyc
19	169.5	13.1	181	10	O9SD02	O9SD02 limnanthes

ALIGNMENTS

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1
RESULT
ID Q9KKE6 PRELIMINARY: PRT: 245 AA.
AC Q9KKE6;
DT 01-OCT-2009 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 27.1 KDA PROTEIN.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
NCBI_TaxID=1718;
[1]
RN
SEQUENCE FROM N.A.
RP STRAIN=ATCC13032;
RA Lee J.K., Park S.Y.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096280; AAF80162.1;
KW Hypothetical protein.
SQ SEQUENCE 245 AA; 27143 MW; 6E87F521A813487B CRC64;

Query Match 100.0%; Score 1298; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. le-108;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MKNWVRLFKYVLIGPLRYVNRPELEGKENIPAEGAAIMASNHAEVMDSFYFPLLCPRQ 60
Db 1 MKNWVRLFKYVLIGPLRYVNRPELEGKENIPAEGAAIMASNHAEVMDSFYFPLLCPRQ 60

QY 61 LTFPPAKAEYFTSPGIKKMKQKWFFTSVGQVPLDRDTADNAMDLSMTAKMVLDRGDLFGIY 120
Db 61 LTFPPAKAEYFTSPGIKKMKQKWFFTSVGQVPLDRDTADNAMDLSMTAKMVLDRGDLFGIY 120

QY 121 PEGSRSPDGRIRYKGTGMAYVAMETGTTVIPAMTIGSRDANPIGSWFEPKPAKVR1KVGSP 180
Db 121 PEGSRSPDGRIRYKGTGMAYVAMETGTTVIPAMTIGSRDANPIGSWFEPKPAKVR1KVGSP 180

QY 181 IDPLAFVCKHGLKPGTYEARKLTDHVMFILADLTGPQYVDAYSKDVKNALEEGKGYPEG 240
Db 181 IDPLAFVCKHGLKPGTYEARKLTDHVMFILADLTGPQYVDAYSKDVKNALEEGKGYPEG 240

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Db 181 IDPLAFVKEHGLKPGTYEARKLTDHVMFLADLTGQPVYDAYSKDVKNALKEEGKGYPEG 240
 QY 241 TAPSO 245
 Db 241 TAPSO 245

RESULT 2
 O69572 PRELIMINARY; PRT; 244 AA.
 AC O69572;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HYPOTHETICAL 26.8 KDA PROTEIN.
 GN MLCB268.24C.

OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brown D., Churcher C.M.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=93188700; PubMed=8446027;
 RA Eiglmeyer K., Honore N., Woods S.A., Caudron B., Cole S.T.;
 RT *Use of an ordered cosmid library to deduce the genomic organization
 RT of Mycobacterium leprae.*;
 RL Mol. Microbiol. 7:197-206(1993).
 DR EMBL; AL022602; CAA18690.1; -;
 DR INTERPRO; IPR002123; -;
 DR PFAM; PF01553; Acyltransferase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 244 AA; 26791 MW; 19F62F7BAC6BBB9 CRC64;

Query Match 44.3%; Score 575; DB 2; Length 244;
 Best Local Similarity 49.6%; Pred. No. 7.7e-44;
 Matches 111; Conservative 41; Mismatches 68; Indels 4; Gaps 2;

QY 5 WYRLFKYVLIGPFLRVNRPETEGKENIPAEAGAAIMASNEHVAVMSFYFPLCPROLTPP 64
 Db 2 WYLFKYIFMGPALSVLGRPKVLEGLYIPSSGPAILASNLAVADSFYLPVVRRIITEL 61
 QY 65 AKAEYFTSPGKQKQWFTSVGVPLDRTADNADSLMTAKWLDKGLDFGIYPEG 124
 Db 62 AKSEYFTGKLGWFTSWFYRATQGVPIIDRTADTAALNTAERLLGKLGIMTPEST 121
 QY 125 RSPDGRYKGTGMAYVAMETGTVIPVAMIGSRDANPTGSWFPKPAKVRKVGSPIDPL 184
 Db 122 RSPDGRYKGTGMAYVAMETGTVIPVAMIGSRDANPTGSWFPKPAKVRKVGSPIDPL 179
 QY 185 APVKEHGLKPGTYEARKLTDHVMFLADLTGQPVYDAYSKDVKNALKEEG 228
 Db 180 -FSRFEGL-AAGNRVIERVITDEVIIYELMELSGQYVDIYAASVK 221

RESULT 3
 O53516 PRELIMINARY; PRT; 247 AA.
 AC O53516;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HYPOTHETICAL 27.0 KDA PROTEIN.
 GN RV2182C OR MT0021.15C.
 OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekai F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krohn A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT *Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.*;
 RL Nature 393:537-544(1998).
 DR EMBL; AL021957; CAA17486.1; -;
 DR TUBERCULIST; RV2182C; -;
 DR INTERPRO; IPR002123; -;
 DR PFAM; PF01553; Acyltransferase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 247 AA; 26955 MW; FB1094228A340BDB CRC64;

Query Match 43.6%; Score 566; DB 2; Length 247;
 Best Local Similarity 47.8%; Pred. No. 5e-43;
 Matches 110; Conservative 43; Mismatches 73; Indels 4; Gaps 2;

QY 5 WYRLFKYVLIGPFLRVNRPETEGKENIPAEAGAAIMASNEHVAVMSFYFPLCPROLTPP 64
 Db 2 WYLFKYIFMGPALSVLGRPKVLEGLYIPSSGPAILASNLAVADSFYLPVVRRIITEL 61
 QY 65 AKAEYFTSPGKQKQWFTSVGVPLDRTADNADSLMTAKWLDKGLDFGIYPEG 124
 Db 62 AKSEYFTGKLGWFTSWFYRATQGVPIIDRTADTAALNTAERLLGKLGIMTPEST 121
 QY 125 RSPDGRYKGTGMAYVAMETGTVIPVAMIGSRDANPTGSWFPKPAKVRKVGSPIDPL 184
 Db 122 RSPDGRYKGTGMAYVAMETGTVIPVAMIGSRDANPTGSWFPKPAKVRKVGSPIDPL 179
 QY 185 APVKEHGLKPGTYEARKLTDHVMFLADLTGQPVYDAYSKDVKNALKEEG 234
 Db 180 -FSRFEGL-AGNHFIERAVTDEVIIYELMELSGQYVDIYAASVKDGRNAG 227

RESULT 4
 O9S2M2 PRELIMINARY; PRT; 262 AA.
 AC O9S2M2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE HYPOTHETICAL 28.2 KDA PROTEIN.
 GN SC6E10.16C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);